

04-24-06

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PTO/SB/21 (6-99)

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Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE

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TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

		Application Number	09/272,835
		Filing Date	March 19, 1999
		First Named Inventor	FREDERIC J. DE SAUVAGE et al.
		Group/Art Unit	1647
		Examiner Name	Robert C. Hayes
Total Number of Pages in This Submission		Attorney Docket No.	39766-0065

ENCLOSURES (check all that apply)

<input type="checkbox"/> Fee Transmittal Form <input type="checkbox"/> Fee Attached <input type="checkbox"/> Amendment <input type="checkbox"/> After Final <input type="checkbox"/> Version With Markings Showing Changes <input type="checkbox"/> Affidavits/declaration(s) <input type="checkbox"/> Extension of Time Request <input type="checkbox"/> Information Disclosure Statement with Form PTO-1449 <input type="checkbox"/> Certified Copy of Priority Document(s) <input type="checkbox"/> Response to Missing Parts/ Incomplete Application <input type="checkbox"/> Response To Missing Parts Under 37 CFR 1.52 Or 1.53 <input type="checkbox"/> Copy Of Notice	<input checked="" type="checkbox"/> Request for Certificate of Correction	<input type="checkbox"/> After Allowance Communication to Group
	<input checked="" type="checkbox"/> Certificate of Correction	<input type="checkbox"/> Appeal Communication to Board of Appeals and Interferences
	<input type="checkbox"/> Assignment	<input type="checkbox"/> Appeal Communication to Group (Appeal Notice, Brief, Reply Brief)
	<input type="checkbox"/> Power of Attorney, Revocation Change of Correspondence Address	<input type="checkbox"/> Proprietary Information
	<input type="checkbox"/> Petition to Convert to a Provisional Application	<input checked="" type="checkbox"/> Additional Enclosure(s) (please identify below):
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	<input type="checkbox"/> Terminal Disclaimer	
	<input type="checkbox"/> Small Entity Status Claimed	
	Remarks AUTHORIZATION TO CHARGE DEPOSIT ACCOUNT 08-1641 FOR ANY FEES DUE IN CONNECTION WITH THIS PAPER.	

Certificate
 APR 27 2006
of Correction

SIGNATURE OF APPLICANT, ATTORNEY OR AGENT

Firm or Individual name	HELLER EHRMAN LLP		JAMES A. FOX, REG. NO.: 38,455	
	275 Middlefield Road, Menlo Park, California 94025		Telephone: (650) 324-7000	Facsimile: (650) 324-0638
Signature				
Date	April 20, 2006	Customer Number:	25213	

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Typed or printed name	Sylvia Rogers		
Signature		Date	April 20, 2006

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SV 2202564 v1

MAY 01 2006



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In application of:

Frederic J. DE SAUVAGE et al.

U.S. Patent No. 7,026,138 ⁸¹

Issued: April 11, 2006

For: **POLYNUCLEOTIDES ENCODING
GFR α 3**

) Examiner: Robert C. HAYES

) Art Unit: 1647

) Application Serial No. 09/272,835

) Filed: March 19, 1999

) Attorney's Docket No. 39766-0065 A

) Customer No. 25213

EXPRESS MAIL LABEL NO. EL 992 477 765 US
DATE MAILED: APRIL 20, 2006

REQUEST FOR CERTIFICATE OF CORRECTION

MAIL STOP CERTIFICATE OF CORRECTIONS BRANCH

Commissioner for Patents
PO Box 1450
Alexandria Virginia 22313-1450

Sir:

Patentee hereby requests a Certificate of Correction.

The requested change replaces the incorrect Sequence Listing as published in U.S. Patent 7,026,138 at columns 59-72 with the correct Sequence Listing as filed and examined in the application. A paper copy of the correct Sequence Listing is enclosed with this Request for a Certificate of Correction.

The nature of the requested correction does not involve changes that would constitute new matter or require reexamination.

The requested correction corrects an error in the published sequence listing in that the published sequence listing is not the Sequence Listing filed with the application and examined by the U.S.P.T.O. with respect to the application. That the published sequence listing is incorrect may be seen by inspection: for example, the correct Sequence Listing includes 25 sequences, while the published sequence listing has only 5 sequences. Further inspection reveals, for example, that the first sequence of the correct Sequence Listing is a DNA sequence from Mus Musculus having 387 nucleic acid residues, while the first sequence of the incorrect published sequence listing is an artificial DNA sequence having 12982 nucleic acid residues.

Patentee therefore submits that this is an appropriate case for a Certificate of Correction. Submitted herewith is a completed Form PTO-1050 containing the requested correction.

MAY 01 2006

A return receipt postcard is enclosed.

Patentee further notes that the Sequence Listings available for inspection via the PAIR system have the correct number of sequences and appear to present the correct Sequence Listing as filed and examined in the application that matured into the present patent.

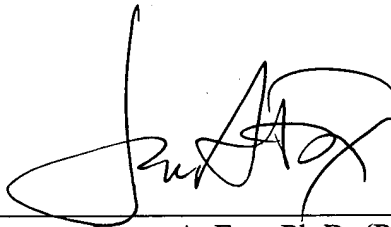
Patentee thus believes this error in publishing the incorrect sequence listing to be a publication error on the part of the United States Patent and Trademark Office, and not due to any error on the part of patentee. Thus, no fees are believed to be due.

However, the Commissioner is authorized to charge the filing fee of **\$100.00** for the Certificate of Correction if the Commissioner deems it to be required, and to charge any additional fees that may be required, or to credit any refund, to Deposit Account No. **08-1641**, referencing Attorney's Docket No. **39766-0065 A**.

Respectfully submitted,

Date: April 20, 2006

By:



James A. Fox, Ph.D. (Reg. No. 38,455)

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SV 2202228 v1
4/20/06 12:58 PM (39766.0065)

MAY 01 2006

UNITED STATES PATENT AND TRADEMARK OFFICE CERTIFICATE OF CORRECTION

PATENT NO. : 7,026,138 **B1**
DATED : April 11, 2006
INVENTOR(S) : Frederic J. de Sauvage et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the SEQUENCE LISTING

Delete the published SEQUENCE LISTING and replace it with the following correct SEQUENCE LISTING

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<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 387

<212> DNA

<213> Mus musculus

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<212> DNA

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MAY 01 2006

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<212> PRT

<213> Mus musculus

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Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	Gly
		420						425				430			
Ser	Asn	Lys	Val	Ile	Lys	Pro	Asn	Ser	Gly	Pro	Ser	Arg	Ala	Arg	Pro
		435					440					445			
Ser	Ala	Ala	Leu	Thr	Val	Leu	Ser	Val	Leu	Met	Leu	Lys	Leu	Ala	Leu
		450				455					460				

<210> 8

<211> 468

<212> PRT

<213> Rattus norvegicus

<400> 8

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu
1				5					10					15	
Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala
		20						25					30		
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
	35					40						45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser
	50					55				60					
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65				70						75				80	
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
			85						90					95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
			100						105					110	
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu
	115							120					125		
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln
	130					135					140				
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala
145					150					155				160	
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr
			165						170					175	
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys
		180						185						190	
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser
	195						200					205			
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg
	210					215					220				
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg
225				230						235				240	
Pro	Asn	Cys	Leu	Ser	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys
			245						250					255	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg
		260						265					270		
Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
	275						280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser
	290				295						300				
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn
305				310						315				320	
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr
			325						330					335	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr
		340						345					350		
Met	Trp	Gln	Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr
	355						360						365		
Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu
	370				375						380				
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala
385				390						395				400	
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	Ser
			405						410					415	
Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	Ile
		420						425				430			
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu
		435					440					445			

Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
 450 455 460
 Ala Glu Thr Ser
 465

<210> 9
 <211> 464
 <212> PRT
 <213> Rattus Norvegicus

<400> 9
 Met Ile Leu Ala Asn Ala Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr
 1 5 10 15
 Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His
 20 25 30
 Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
 35 40 45
 Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
 50 55 60
 Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
 65 70 75 80
 Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
 85 90 95
 Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
 100 105 110
 His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
 115 120 125
 Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
 130 135 140
 Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His
 145 150 155 160
 Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
 165 170 175
 Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
 180 185 190
 Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
 195 200 205
 Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
 210 215 220
 Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
 225 230 235 240
 Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Ser
 245 250 255
 Leu Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
 260 265 270
 Ala Asn Cys Arg Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp
 275 280 285
 Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
 290 295 300
 Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser
 305 310 315 320
 Pro Trp Cys Asn Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
 325 330 335
 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
 340 345 350
 Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro
 355 360 365
 Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
 370 375 380

Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
 385 390 395 400
 Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
 405 410 415
 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly
 420 425 430
 Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu
 435 440 445
 Ser Ala Ala Leu Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu
 450 455 460

<210> 10
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
 <222> (0)...(0)
 <223> n = A, T, C or G

<400> 10
 ggcgtgnntg ncngnangng ggggcgggag gtgccgggtcg agggagcccc gctctcagag 60
 ctccagggga ggagcgangg gagcgcgag cccggcgcc tacagctcgc catgggtgcgc 120
 cccctgaacc cgcgaccgct gccgcccgtg gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
 nnnnnnnngc ctctcgcagc cggagacccc ttccacacag aaagccgact catgaacagc 240
 tgtctccagg ccaggaggaa gtgccaggct gatccacact gc 282

<210> 11
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcctctcgca gccggagacc 20

<210> 12
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 12
 caggtgggat cagcctggca c 21

<210> 13
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 13
 tctcgagcc ggagaccccc ttccacaga aagccgactc a 41

<210> 14
 <211> 1792
 <212> DNA
 <213> Homo sapiens

<400> 14

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atgaacagct gtctccaggc caggaggaag tgccaggctg atcccacctg cagtgtgtgcc 180
taccaccacc tggattcctg cactcttagc ataagcacc cactgccctc agaggagcct 240
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tgcattgtgcc accggcgcat gaagaaccag gttgcctgct tggacatcta ttggaccggt 360
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accagcaaac cctggaaaat gaatctcagc aaactgaaca tgctcaaacc agactcagac 480
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gcctacgggg aggcgtgtct cgggccccac tgccagcgcc acgtctgctt caggcagctg 600
ctcactttct tcgagaaggc cgccgagccc cagcgcaggg gctgtctact gtgcccattg 660
gcccccaacg accggggctg cggggagcgc cggcgcaaca ccacgcgcc caactgcgcg 720
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agaatctaata agtttagcct ttctctattg cattccagat taggggttagg gtaggaggga 1560
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<210> 15

<211> 400

<212> PRT

<213> Homo Sapiens

<400> 15

```

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1          5          10          15
Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20          25          30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35          40          45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
50          55          60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65          70          75          80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85          90          95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100         105         110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
115         120         125
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130         135         140
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145         150         155         160
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165         170         175
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln

```

	180		185		190
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala					
195		200		205	
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp					
210		215		220	
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala					
225		230		235	240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe					
	245		250		255
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys					
	260		265		270
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys					
	275		280		285
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe					
	290		295		300
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly					
305		310		315	320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser					
	325		330		335
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His					
	340		345		350
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met					
	355		360		365
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro					
	370		375		380
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp					
385		390		395	400

<210> 16

<211> 1837

<212> DNA

<213> Homo sapeins

<400> 16

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gcccggcgcc  tacagctcgc  catggtgcgc  cccctgaacc  cgcgaccgct  gccgcccgta  180
gtcctgatgt  tgctgtctgt  gctgccgccc  tcgccgtgct  ctctcgcagc  cggagacccc  240
cttcccacag  aaagccgact  catgaacagc  tgtctccagg  ccaggaggaa  gtgccaggct  300
gatccacact  gcagtgtctg  ctaccaccac  ctggattcct  gcacctctag  cataagcacc  360
ccactgccct  cagaggagcc  ttcggtcctt  gctgactgcc  tggaggcagc  acagcaactc  420
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gcgtgtctcc  ggccccactg  ccagcgccac  gtctgcctca  ggcagctgct  cactttcttc  660
gagaaggccg  ccgagcccca  cgcgcagggc  ctgctactgt  gcccatgtgc  ccccaacgac  720
cggggctgcg  gggagcgccg  gcgcaacacc  atcgccccc  actgcgcgct  gccgctgtg  780
gcccccaact  gcctggagct  gcggcgcttc  tgcttctccg  acccgctttg  cagatcacgc  840
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cagtcagat  gtctacgagc  atacctgggg  ctgattggga  ctgccatgac  ccccaacttt  960
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tttgctgtga  tggcacacca  gaatgaaaac  cctgtgtga  ggccacagcc  ctgggtgccc  1200
tctcttttct  cctgcacgct  tcccttgatt  ctgctcctga  gcctatggta  gctggacttc  1260
cccaggggccc  tcttcccctc  caccacaccc  aggtggactt  gcagcccaca  aggggtgagg  1320
aaaggacagc  agcaggaagg  aggtgcagtg  cgcagatgag  ggcacaggag  aagctaaggg  1380
ttatgacctc  cagatcctta  ctggtccagt  cctcattccc  tccaccccat  ctccacttct  1440
gattcatgct  gccctcctt  ggtggccaca  atttagccat  gtcacttggt  ggtgaccagc  1500

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tccaccaagc ccctttctga gcccttctc ttgactacca ggatcaccag aatctaataa 1560
gtagccttt ctctattgca ttccagatta gggtaggggt agggaggact ggggtgttctg 1620
aggcagccta gaaagtcatt ctcccttctg aagaaggctc ctgccccctc gtctcctcct 1680
ctgagtggag gatggaaaac tactgcctgc actgccctgt ccccgatcc tgcgaacat 1740
ctgggcatca ggagctggag cctgtgggccc ttgctttatt cctattattg tcctaaagtc 1800
tctctgggct cttggatcat gattaaacct ttgactt 1837

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<210> 17
<211> 369
<212> PRT
<213> Homo sapiens

```

<400> 17

```

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1          5          10          15
Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20          25          30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35          40          45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
50          55          60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65          70          75          80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85          90          95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100         105         110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Asp Ser
115         120         125
Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys
130         135         140
Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys
145         150         155         160
Gln Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala
165         170         175
Ala Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn
180         185         190
Asp Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys
195         200         205
Ala Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys
210         215         220
Phe Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His
225         230         235         240
Cys His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg
245         250         255
Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn
260         265         270
Phe Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg
275         280         285
Gly Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe
290         295         300
Ser His Asn Pro Cys Leu Thr Glu Ala Ile Ala Lys Met Arg Phe
305         310         315         320
His Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val
325         330         335
Met Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val
340         345         350
Pro Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu
355         360         365
Trp

```

<210> 18
 <211> 628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric receptor comprising human sequence.

<400> 18

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25					30		
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
	35					40					45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
50					55				60						
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70				75						80
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
			85					90					95		
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
	115					120					125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
130						135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145					150					155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
			165					170					175		
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
	195						200					205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
210						215					220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
225					230					235					240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
			245					250					255		
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
			260					265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
	275						280					285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
290						295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
			325					330					335		
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340					345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
	355						360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
370						375					380				

Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
 385 390 395 400
 Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 405 410 415
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 420 425 430
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 435 440 445
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 450 455 460
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 465 470 475 480
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 485 490 495
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 500 505 510
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 515 520 525
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 530 535 540
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 545 550 555 560
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 565 570 575
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 580 585 590
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 595 600 605
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 610 615 620
 Ser Pro Gly Lys
 625

<210> 19

<211> 951

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor comprising rat sequence.

<400> 19

Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
 1 5 10 15
 Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20 25 30
 Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45
 Val Leu Asp Gln Leu Leu Glu Pro Ser Ser Leu Gln Gly Ser Glu Leu
 50 55 60
 His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys
 65 70 75 80
 Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys
 85 90 95
 Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln
 100 105 110
 Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys
 115 120 125
 Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser

130	Ile His Leu Gly Leu Thr	135	Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro
145	Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser	150	155
	165	170	175
Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn	180	185	190
His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys	195	200	205
Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro	210	215	220
Thr Glu Arg Cys Asn Arg Lys Cys His Lys Ala Leu Arg Gln Phe	225	230	235
Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser	245	250	255
Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro	260	265	270
Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg	275	280	285
Ser Leu Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe	290	295	300
His Ala Asn Cys Arg Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala	305	310	315
Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe	325	330	335
Asp Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val	340	345	350
Ser Pro Trp Cys Asn Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys	355	360	365
Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala	370	375	380
Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly	385	390	395
Pro Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser	405	410	415
Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile	420	425	430
Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser	435	440	445
Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro	450	455	460
Gly Trp Arg Ala Trp Val Pro Val Val Leu Gly Val Leu Thr Ala Leu	465	470	475
Val Thr Ala Ala Ala Leu Ala Leu Ile Leu Leu Arg Lys Arg Arg Lys	485	490	495
Glu Thr Arg Phe Gly Gln Ala Phe Asp Ser Val Met Ala Arg Gly Glu	500	505	510
Pro Ala Val His Phe Arg Ala Ala Arg Ser Phe Asn Arg Glu Arg Pro	515	520	525
Glu Arg Ile Glu Ala Thr Leu Asp Ser Leu Gly Ile Ser Asp Glu Leu	530	535	540
Lys Glu Lys Leu Glu Asp Val Leu Ile Pro Glu Gln Gln Phe Thr Leu	545	550	555
Gly Arg Met Leu Gly Lys Gly Glu Phe Gly Ser Val Arg Glu Ala Gln	565	570	575
Leu Lys Gln Glu Asp Gly Ser Phe Val Lys Val Ala Val Lys Met Leu	580	585	590
Lys Ala Asp Ile Ile Ala Ser Ser Asp Ile Glu Glu Phe Leu Arg Glu	595	600	605
Ala Ala Cys Met Lys Glu Phe Asp His Pro His Val Ala Lys Leu Val			

610	615	620
Gly Val Ser Leu Arg Ser Arg Ala Lys Gly Arg Leu Pro Ile Pro Met		
625	630	635
Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ala Phe Leu Leu		640
	645	650
Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln Thr Leu		655
	660	665
Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr Leu Ser Ser		670
	675	680
Arg Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Ala		685
	690	695
Glu Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Arg Lys Ile		700
705	710	715
Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Cys Ala Ser Lys Leu Pro Val		720
	725	730
Lys Trp Leu Ala Leu Glu Ser Leu Ala Asp Asn Leu Tyr Thr Val Gln		735
	740	745
Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Met Thr Arg		750
	755	760
Gly Gln Thr Pro Tyr Ala Gly Ile Glu Asn Ala Glu Ile Tyr Asn Tyr		765
	770	775
Leu Ile Gly Gly Asn Arg Leu Lys Gln Pro Pro Glu Cys Met Glu Asp		780
785	790	795
Val Tyr Asp Leu Met Tyr Gln Cys Trp Ser Ala Asp Pro Lys Gln Arg		800
	805	810
Pro Ser Phe Thr Cys Leu Arg Met Glu Leu Glu Asn Ile Leu Gly Gln		815
	820	825
Leu Ser Val Leu Ser Ala Ser Gln Asp Pro Leu Tyr Ile Asn Ile Glu		830
	835	840
Arg Ala Glu Glu Pro Thr Ala Gly Gly Ser Leu Glu Leu Pro Gly Arg		845
	850	855
Asp Gln Pro Tyr Ser Gly Ala Gly Asp Gly Ser Gly Met Gly Ala Val		860
865	870	875
Gly Gly Thr Pro Ser Asp Cys Arg Tyr Ile Leu Thr Pro Gly Gly Leu		880
	885	890
Ala Glu Gln Pro Gly Gln Ala Glu His Gln Pro Glu Ser Pro Leu Asn		895
	900	905
Glu Thr Gln Arg Leu Leu Leu Leu Gln Gln Gly Leu Leu Pro His Ser		910
	915	920
Ser Cys Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg		925
	930	935
Gly Lys Asp Leu Pro Val Leu		940
945	950	

<210> 20

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor comprising murine sequence.

<400> 20

Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val		
1	5	10
Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala		15
	20	25
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro		30
	35	40
		45

Val	Leu	Asp	Gln	Leu	Leu	Glu	Ala	Gly	Asn	Ser	Leu	Ala	Thr	Glu	Asn	50	55	60
Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys	Glu	Ala	Asn	65	70	75
Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Gly	Ser	Cys	Thr	Ser	Ser	85	90	95
Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser	Ala	Asp	Cys	100	105	110
Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Asp	Cys	Arg	115	120	125
Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp	Ile	Tyr	Trp	130	135	140
Thr	Val	His	Pro	Ala	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu	Asp	Val	Ser	145	150	155
Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	Leu	Ser	165	170	175
Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	Phe	Ala	180	185	190
Met	Leu	Cys	Thr	Leu	His	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	Ala	Tyr	195	200	205
Gly	Glu	Ala	Cys	Ser	Gly	Ile	Arg	Cys	Gln	Arg	His	Leu	Cys	Leu	Ala	210	215	220
Gln	Leu	Arg	Ser	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Ser	His	Ala	Gln	Gly	225	230	235
Leu	Leu	Leu	Cys	Pro	Cys	Pro	Pro	Glu	Asp	Ala	Gly	Cys	Gly	Glu	Arg	245	250	255
Arg	Arg	Asn	Thr	Ile	Ala	Pro	Ser	Cys	Ala	Leu	Pro	Ser	Val	Thr	Pro	260	265	270
Asn	Cys	Leu	Asp	Leu	Arg	Ser	Phe	Cys	Arg	Ala	Asp	Pro	Leu	Cys	Arg	275	280	285
Ser	Arg	Leu	Met	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	Leu	290	295	300
Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	Gly	305	310	315
Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Ile	Ser	Lys	Val	Asn	Thr	325	330	335
Thr	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	Asp	340	345	350
Glu	Cys	Glu	Gln	Leu	Glu	Arg	Ser	Phe	Ser	Gln	Asn	Pro	Cys	Leu	Val	355	360	365
Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Arg	Gln	Leu	Phe	Ser	Gln	370	375	380
Asp	Trp	Ala	Asp	Ser	Thr	Phe	Ser	Val	Val	Gln	Gln	Gln	Asn	Ser	Asn	385	390	395
Pro	Ala	Trp	Arg	Ala	Trp	Val	Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	405	410	415
Leu	Val	Thr	Ala	Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	420	425	430
Lys	Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	435	440	445
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	Arg	Glu	Arg	450	455	460
Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	465	470	475
Leu	Lys	Glu	Lys	Leu	Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	485	490	495
Leu	Gly	Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	500	505	510
Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	Lys	Met	515	520	525

Leu Lys Ala Asp Ile Ile Ala Ser Ser Asp Ile Glu Glu Phe Leu Arg
 530 535 540
 Glu Ala Ala Cys Met Lys Glu Phe Asp His Pro His Val Ala Lys Leu
 545 550 555 560
 Val Gly Val Ser Leu Arg Ser Arg Ala Lys Gly Arg Leu Pro Ile Pro
 565 570 575
 Met Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ala Phe Leu
 580 585 590
 Leu Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln Thr
 595 600 605
 Leu Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr Leu Ser
 610 615 620
 Ser Arg Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu
 625 630 635 640
 Ala Glu Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Arg Lys
 645 650 655
 Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Cys Ala Ser Lys Leu Pro
 660 665 670
 Val Lys Trp Leu Ala Leu Glu Ser Leu Ala Asp Asn Leu Tyr Thr Val
 675 680 685
 Gln Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Met Thr
 690 695 700
 Arg Gly Gln Thr Pro Tyr Ala Gly Ile Glu Asn Ala Glu Ile Tyr Asn
 705 710 715 720
 Tyr Leu Ile Gly Gly Asn Arg Leu Lys Gln Pro Pro Glu Cys Met Glu
 725 730 735
 Asp Val Tyr Asp Leu Met Tyr Gln Cys Trp Ser Ala Asp Pro Lys Gln
 740 745 750
 Arg Pro Ser Phe Thr Cys Leu Arg Met Glu Leu Glu Asn Ile Leu Gly
 755 760 765
 Gln Leu Ser Val Leu Ser Ala Ser Gln Asp Pro Leu Tyr Ile Asn Ile
 770 775 780
 Glu Arg Ala Glu Glu Pro Thr Ala Gly Gly Ser Leu Glu Leu Pro Gly
 785 790 795 800
 Arg Asp Gln Pro Tyr Ser Gly Ala Gly Asp Gly Ser Gly Met Gly Ala
 805 810 815
 Val Gly Gly Thr Pro Ser Asp Cys Arg Tyr Ile Leu Thr Pro Gly Gly
 820 825 830
 Leu Ala Glu Gln Pro Gly Gln Ala Glu His Gln Pro Glu Ser Pro Leu
 835 840 845
 Asn Glu Thr Gln Arg Leu Leu Leu Leu Gln Gln Gly Leu Leu Pro His
 850 855 860
 Ser Ser Cys Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg Phe
 865 870 875 880
 Arg Gly Lys Asp Leu Pro Val Leu
 885

<210> 21
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 21
 gcgaggggag cgcggagccc ggcgcctaca gctcggc

37

<210> 22
 <211> 20
 <212> DNA
 <213> Mus musculus

<400> 22
gcccgcgacc tccactgctg

20

<210> 23
<211> 18
<212> DNA
<213> Mus musculus

<400> 23
ctgtggggag cggcggcg

18

<210> 24
<211> 20
<212> DNA
<213> Mus musculus

<400> 24
cctgaaccta tggttaactgg

20

<210> 25
<211> 17
<212> DNA
<213> Mus musculus

<400> 25
accagtcct ccctacc

17

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